PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/380,051*

AU 1812

DATE: 06/20/95
TIME: 12:01:38

INPUT SET: S4268.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
 1                          SEQUENCE LISTING
 2
 3   (1)     General Information:
 4
 5       (i)   APPLICANT:                MUKHERJEE, RANJAN
 6
 7       (ii)  TITLE OF INVENTION:       Human Peroxisome
 8                                       Proliferator Activated
 9                                       Receptor y
10
11   (iii)  NUMBER OF SEQUENCES:       2
12
13    (iv)  CORRESPONDENCE ADDRESS:
14
15            (A)   ADDRESSEE:          Lyon & Lyon
16            (B)   STREET:             633 West Fifth Street
17                                      Suite 4700
18            (C)   CITY:               Los Angeles
19            (D)   STATE:              California
20            (E)   COUNTRY:            U.S.A.
21            (F)   ZIP:                90071-2066
22
23
24     (v)   COMPUTER READABLE FORM:
25
26            (A)   MEDIUM TYPE:        3.5" Diskette, 1.44 Mb
27                                      storage
28            (B)   COMPUTER:           IBM Compatible
29            (C)   OPERATING SYSTEM:   IBM P.C. DOS 5.0
30            (D)   SOFTWARE:           Word Perfect 5.1
31
32
33    (vi)   CURRENT APPLICATION DATA:
34
35            (A)   APPLICATION NUMBER: 08/380,051
36            (B)   FILING DATE:        January 30, 1995
37            (C)   CLASSIFICATION:
38
39
40  (viii)   ATTORNEY/AGENT INFORMATION:
41
42            (A)   NAME:               Warburg, Richard J.
43            (B)   REGISTRATION NUMBER: 32,327
44            (C)   REFERENCE/DOCKET NUMBER: 210/100
45
46
```

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INPUT SET: S4268.raw

47   (ix) TELECOMMUNICATION INFORMATION:
48
49   (A) TELEPHONE: (213) 489-1600
50   (B) TELEFAX: (213) 955-0440
51   (C) TELEX: 67-3510
52
53
54
55
56 (2) INFORMATION FOR SEQ ID NO: 1:
57
58   (i) SEQUENCE CHARACTERISTICS:
59
60   (A) LENGTH: 1641 base pairs
61   (B) TYPE: nucleic acid
62   (C) STRANDEDNESS: single
63   (D) TOPOLOGY: linear
64
65   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
66
67 GAATTCCGGA CCCTCAACAC CACTCCCTCT TAGCCAATAT TGTGCCTATT 50
68
69 GCCATACTAG TCTTTGCGCC TGCGAAGCAG CGGTGGCCTA GCCCTACTAG 100
70
71 TCTCAATCTC CAACATATAT CGGCCTAGAC TACGTACATA ACCTAAACCT 150
72
73 ACTCCAATGC TAAAACTAAT CGTCCCTTTT CTCAAACGAG AGTCAGCCTT 200
74
75 TAACGAAATG ACCATGGTTG ACACAGAGAT GCCATTCTGG CCCACCAACT 250
76
77 TTGGGATCAG CTCCGTGGAT CTCTCCGTAA TGGAAGACCA CTCCCACTCC 300
78
79 TTTGATATCA AGCCCTTCAC TACTGTTGAC TTCTCCAGCA TTTCTACTCC 350
80
81 ACATTACGAA GACATTCCAT TCACAAGAAC AGATCCAGTG GTTGCAGATT 400
82
83 ACAAGTATGA CCTGAAACTT CAAGAGTACC AAAGTGCAAT CAAAGTGGAG 450
84
85 CCTGCATCTC CACCTTATTA TTCTGAGAAG ACTCAGCTCT ACAATAAGCC 500
86
87 TCATGAAGAG CCTTCCAACT CCCTCATGGC AATTGAATGT CGTGTCTGTG 550
88
89 GAGATAAAGC TTCTGGATTT CACTATGGAG TTCATGCTTG TGAAGGATGC 600
90
91 AAGGGTTTCT TCCGGAGAAC AATCAGATTG AAGCTTATCT ATGACAGATG 650
92
93 TGATCTTAAC TGTCGGATCC ACAAAAAAAG TAGAAATAAA TGTCAGTACT 700
94
95 GTCGGTTTCA GAAATGCCTT GCAGTGGGGA TGTCTCATAA TGCCATCAGG 750
96
97 TTTGGGCGGA TGCCACAGGC CGAGAAGGAG AAGCTGTTGG CGGAGATCTC 800
98
99 CAGTGATATC GACCAGCTGA ATCCAGAGTC CGCTGACCTC CGGGCCCTGG 850

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/380,051*

INPUT SET: S4268.raw

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100
101    CAAAACATTT GTATGACTCA TACATAAAGT CCTTCCCGCT GACCAAAGCA  900
102
103    AAGGCGAGGG CGATCTTGAC AGGAAAGACA ACAGACAAAT CACCATTCGT  950
104
105    TATCTATGAC ATGAATTCCT TAATGATGGG AGAAGATAAA ATCAAGTTCA  1000
106
107    AACACATCAC CCCCCTGCAG GAGCAGAGCA AAGAGGTGGC CATCCGCATC  1050
108
109    TTTCAGGGCT GCCAGTTTCG CTCCGTGGAG GCTGTGCAGG AGATCACAGA  1100
110
111    GTATGCCAAA AGCATTCCTG GTTTTGTAAA TCTTGACTTG AACGACCAAG  1150
112    TAACTCTCCT CAAATATGGA GTCCACGAGA TCATTTACAC AATGCTGGCC  1200
113
114    TCCTTGATGA ATAAAGATGG GGTTCTCATA TCCGAGGGCC AAGGCTTCAT  1250
115
116    GACAAGGGAG TTTCTAAAGA GCCTGCGAAA GCCTTTTGGT GACTTTATGG  1300
117
118    AGCCCAAGTT TGAGTTTGCT GTGAAGTTCA ATGCACTGGA ATTAGATGAC  1350
119
120    AGCGACTTGG CAATATTTAT TGCTGTCATT ATTCTCAGTG GAGACCGCCC  1400
121
122    AGGTTTGCTG AATGTGAAGC CCATTGAAGA CATTCAAGAC AACCTGCTAC  1450
123
124    AAGCCCTGGA GCTCCAGCTG AAGCTGAACC ACCCTGAGTC CTCACAGCTG  1500
125
126    TTTGCCAAGC TGCTCCAGAA AATGACAGAC CTCAGACAGA TTGTCACGGA  1550
127
128    ACACGTGCAG CTACTGCAGG TGATCAAGAA GACGGAGACA GACATGAGTC  1600
129
130    TTCACCCGCT CCTGCAGGAG ATCTACAAGG ACTTGTACTA G            1641
131
132
133
134
135
136    (2) INFORMATION FOR SEQ ID NO:    2:
137
138            (i) SEQUENCE CHARACTERISTICS:
139
140                (A) LENGTH:         494 amino acids
141                (B) TYPE:           amino acid
142                (C) STRANDEDNESS:     single
143                (D) TOPOLOGY:       linear
144
145           (ii) MOLECULE TYPE:  peptide
146
147           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
148
149    Met Leu Lys Leu Ile Val Pro Phe Leu Lys Arg Glu Ser Ala Phe
150                     5                  10                  15
151
152
```

```
153   Asn Glu Met Thr Met Val Asp Thr Glu Met Pro Phe Trp Pro Thr
154               20              25              30
155
156   Asn Phe Gly Ile Ser Ser Val Asp Leu Ser Val Met Glu Asp His
157               35              40              45
158
159   Ser His Ser Phe Asp Ile Lys Pro Phe Thr Thr Val Asp Phe Ser
160               50              55              60
161
162   Ser Ile Ser Thr Pro His Tyr Glu Asp Ile Pro Phe Thr Arg Thr
163               65              70              75
164
165   Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp Leu Lys Leu Gln Glu
166               80              85              90
167
168   Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser Pro Pro Tyr Tyr
169               95              100             105
170
171   Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu Glu Pro Ser
172               110             115             120
173
174   Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp Lys Ala
175               125             130             135
176
177   Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly
178               140             145             150
179
180   Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys
181               155             160             165
182
183   Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln
184               170             175             180
185
186   Tyr Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn
187               185             190             195
188
189   Ala Ile Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu
190               200             205             210
191
192   Leu Ala Glu Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser
193               215             220             225
194
195   Ala Asp Leu Arg Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile
196               230             235             240
197
198   Lys Ser Phe Pro Leu Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr
199               245             250             255
200
201   Gly Lys Thr Thr Asp Lys Ser Pro Phe Val Ile Tyr Asp Met Asn
202               260             265             270
203
204   Ser Leu Met Met Gly Glu Asp Lys Ile Lys Phe Lys His Ile Thr
205               275             280             285
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```
206
207   Pro Leu Gln Glu Gln Ser Lys Glu Val Ala Ile Arg Ile Phe Gln
208               290           295               300
209
210   Gly Cys Gln Phe Arg Ser Val Glu Ala Val Gln Glu Ile Thr Glu
211               305           310               315
212
213   Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn Leu Asp Leu Asn Asp
214               320           325               330
215
216   Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu Ile Ile Tyr Thr
217               335           340               345
218
219   Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu Ile Ser Glu
220               350           355               360
221
222   Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu Arg Lys
223               365           370               375
224   Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val Lys
225               380           385               390
226
227   Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile
228               395           400               405
229
230   Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val
231               410           415               420
232
233   Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu
234               425           430               435
235
236   Leu Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala
237               440           445               450
238
239   Lys Leu Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu
240               455           460               465
241
242   His Val Gln Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met
243               470           475               480
244
245   Ser Leu His Pro Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr
246               485           490
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/08/380,051*

INPUT SET: S4268.raw

Line   Error   Original Text